



SEQUENCE LISTING

<110> HERING, THOMAS M.
JOHNSTONE, BRIAN

<120> PROBES FOR CHONDROGENESIS

<130> 27708/04065

<140> 10/623,914

<141> 2003-07-21

<150> 60/211,384

<151> 2000-06-14

<160> 7

<170> PatentIn Ver. 3.3

<210> 1

<211> 2666

<212> DNA

<213> Homo sapiens

<400> 1

aatggagcga	agaccatggg	gactgagtac	acagatgaag	acacagaagc	atagagagga	60
taagtaatca	ctagcaagt	gaagaaccgg	gattcagatc	cagaacaggc	tgactccaga	120
gtcactggct	gtcatgtagt	ttcctcaact	actgcctcag	ctctacaatc	ccagagtaaa	180
gctctttctcc	aaatgaagag	ccaggaagag	gtagagggtg	caggaattaa	actttgtaaa	240
gccatgtccc	tgggttcact	gactttcaca	gatgtggcca	tagacttttc	ccaagatgaa	300
tgggagtggc	tgaatcttgc	tcagagaagt	ttgtacaaga	aggtgatgtt	agaaaactac	360
aggaacctag	tttcagtggg	tctttgcatt	tctaaaccag	atgtgatctc	cttactggag	420
caagagaaa	acccttgggt	gataaaaagga	gggatgaaca	gaggcctgtg	cccagacttg	480
gagtgtgtgt	gggtgaccaa	atcattatct	ttaaaccagg	atatttatga	agaaaaatta	540
cccccgcaa	tcataatgga	aagacttaaa	agctatgacc	ttgaatgttc	aacattaggg	600
aaaaactgga	aatgtgaaga	cttgtttgag	agggagcttg	taaaccagaa	gacacatttt	660
aggcaagaga	ccatcactca	tatagatact	cttattgaaa	aaagagatca	ctctaacaaa	720
tctgggacag	tttttcatct	gaatacatta	tcttatataa	aacagatttt	tcccatggaa	780
gagagaatat	ttaattttca	tacagataag	aaaagcttaa	aaacacattc	agttgtgaaa	840
aaacacaagc	aagaccgtgg	agaaaaagaa	cttttaaaat	gtaatgactg	tgagaaaata	900
ttcagcaaaa	tctcaaccct	tactcttcac	caaagaattc	atacaggaga	gaaaccctat	960
gaatgtattg	aatgtggaaa	ggccttttagc	cagagtggcc	accttgctca	acatcagaga	1020
atacacacag	gagaaaaaac	ttttgaatgt	actgaatgtg	ggaaagcctt	cagccagaat	1080
gctcatcttg	ttcaacacca	gagagtccat	actggagaga	aaccttatca	gtgtaagcag	1140
tgtataaaag	cattcagcca	gcttgcacac	cttgctcaac	atcagagggt	ccacactgga	1200
gagaaaccct	atgaatgtat	tgaatgtggg	aaggctttta	gtgattgctc	atccctagct	1260
catcatcgaa	ggattcacac	tgggaaaaga	ccttatgaat	gtattgactg	tgggaaagct	1320
ttcaggcaga	atgcttctct	tatacgtcat	cggcgatatt	atcatactgg	agagaaaccc	1380
tttgactgta	ttgattgtgg	gaaggctttc	actgatcaca	taggacttat	tcagcataag	1440
agaattcata	ctggagagag	accttacaaa	tgtaatgtgt	gtgggaaggc	ttttagccat	1500
ggctcatctc	tgacagtaca	tcagagaatt	catcacaggag	agaaacctta	tgaatgcaat	1560
atctgtgaga	aagccttcag	ccatcggtgg	tctcttactc	ttcatcagag	agttcatact	1620
ggagagaaa	cctatgaatg	taaagaatgt	gggaaagcct	tccggcagag	cacgcattctg	1680
gctcatcatc	agagaattca	tactggagag	aaaccttatg	aatgtaagga	atgcagcaaa	1740
accttcagcc	agaatgcaca	cctcgcgcag	catcagaaaa	tacacactgg	ggagaagcct	1800
tatgaatgta	aggaacgtgg	taaggccttc	agtcagattg	cacaccttgt	tcagcaccag	1860
agagttcata	ctggtgagaa	gccttacgaa	tgtattgaat	gtgggaaggc	ctttagtgat	1920
ggctcatatc	ttgttcaaca	tccgagactc	cacagtggca	aaagaccgta	tgaatgtctt	1980

```

gaatgtggga aggcattcag gcagagggca tccttgattt gtcatcagag atgtcatact 2040
ggtgagaaac cttatgaatg taatgtttgt gggaaagcct ttagccatcg taaatccctt 2100
actctgcatc agagaattca tacaggagag aaaccttatg agtgtaagga atgtagcaaa 2160
gccttcagcc aggttgccca tcttactcta cataagagaa ttcatactgg agaaaggccc 2220
tatgagtgtg aagaatgtgg aaaagccttc aggcagagtg tacatcttgc tcatcatcag 2280
cgaattcata ccggagagtc atcagttatt ctctcctctg ccctcccata ccaccaagtc 2340
ctatagattc aatctcgtaa atgcttctag catccatctg cttttttcca gcacatgtcc 2400
catcatcata gtccaagacg caaccatctc atctggattt ctgcagtagc ataactgttg 2460
ccccctttgc ttctatcaac tacatgttta acactgtagg cagcctaacc ttttaaaaat 2520
aaaaatacat aatttatgtt attttcccat ttaaaacact tgatttgaaa aatatattaa 2580
ctaattccatt tcaaggattt agcacacact ggcatatagt tattgctaaa taaatgctag 2640
ccattaaggt aaaaaaaaaa aaaaaa 2666

```

<210> 2
 <211> 717
 <212> PRT
 <213> Homo sapiens

```

<400> 2
Met Lys Ser Gln Glu Glu Val Glu Val Ala Gly Ile Lys Leu Cys Lys
 1             5             10             15

Ala Met Ser Leu Gly Ser Leu Thr Phe Thr Asp Val Ala Ile Asp Phe
      20             25             30

Ser Gln Asp Glu Trp Glu Trp Leu Asn Leu Ala Gln Arg Ser Leu Tyr
      35             40             45

Lys Lys Val Met Leu Glu Asn Tyr Arg Asn Leu Val Ser Val Gly Leu
      50             55             60

Cys Ile Ser Lys Pro Asp Val Ile Ser Leu Leu Glu Gln Glu Lys Asp
      65             70             75             80

Pro Trp Val Ile Lys Gly Gly Met Asn Arg Gly Leu Cys Pro Asp Leu
      85             90             95

Glu Cys Val Trp Val Thr Lys Ser Leu Ser Leu Asn Gln Asp Ile Tyr
      100            105            110

Glu Glu Lys Leu Pro Pro Ala Ile Ile Met Glu Arg Leu Lys Ser Tyr
      115            120            125

Asp Leu Glu Cys Ser Thr Leu Gly Lys Asn Trp Lys Cys Glu Asp Leu
      130            135            140

Phe Glu Arg Glu Leu Val Asn Gln Lys Thr His Phe Arg Gln Glu Thr
      145            150            155            160

Ile Thr His Ile Asp Thr Leu Ile Glu Lys Arg Asp His Ser Asn Lys
      165            170            175

Ser Gly Thr Val Phe His Leu Asn Thr Leu Ser Tyr Ile Lys Gln Ile
      180            185            190

Phe Pro Met Glu Glu Arg Ile Phe Asn Phe His Thr Asp Lys Lys Ser
      195            200            205

```

Leu Lys Thr His Ser Val Val Lys Lys His Lys Gln Asp Arg Gly Glu
 210 215 220
 Lys Lys Leu Leu Lys Cys Asn Asp Cys Glu Lys Ile Phe Ser Lys Ile
 225 230 235 240
 Ser Thr Leu Thr Leu His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr
 245 250 255
 Glu Cys Ile Glu Cys Gly Lys Ala Phe Ser Gln Ser Ala His Leu Ala
 260 265 270
 Gln His Gln Arg Ile His Thr Gly Glu Lys Pro Phe Glu Cys Thr Glu
 275 280 285
 Cys Gly Lys Ala Phe Ser Gln Asn Ala His Leu Val Gln His Gln Arg
 290 295 300
 Val His Thr Gly Glu Lys Pro Tyr Gln Cys Lys Gln Cys Asn Lys Ala
 305 310 315 320
 Phe Ser Gln Leu Ala His Leu Ala Gln His Gln Arg Val His Thr Gly
 325 330 335
 Glu Lys Pro Tyr Glu Cys Ile Glu Cys Gly Lys Ala Phe Ser Asp Cys
 340 345 350
 Ser Ser Leu Ala His His Arg Arg Ile His Thr Gly Lys Arg Pro Tyr
 355 360 365
 Glu Cys Ile Asp Cys Gly Lys Ala Phe Arg Gln Asn Ala Ser Leu Ile
 370 375 380
 Arg His Arg Arg Tyr Tyr His Thr Gly Glu Lys Pro Phe Asp Cys Ile
 385 390 395 400
 Asp Cys Gly Lys Ala Phe Thr Asp His Ile Gly Leu Ile Gln His Lys
 405 410 415
 Arg Ile His Thr Gly Glu Arg Pro Tyr Lys Cys Asn Val Cys Gly Lys
 420 425 430
 Ala Phe Ser His Gly Ser Ser Leu Thr Val His Gln Arg Ile His Thr
 435 440 445
 Gly Glu Lys Pro Tyr Glu Cys Asn Ile Cys Glu Lys Ala Phe Ser His
 450 455 460
 Arg Gly Ser Leu Thr Leu His Gln Arg Val His Thr Gly Glu Lys Pro
 465 470 475 480
 Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Gln Ser Thr His Leu
 485 490 495
 Ala His His Gln Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys
 500 505 510

Glu Cys Ser Lys Thr Phe Ser Gln Asn Ala His Leu Ala Gln His Gln
 515 520 525
 Lys Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Arg Gly Lys
 530 535 540
 Ala Phe Ser Gln Ile Ala His Leu Val Gln His Gln Arg Val His Thr
 545 550 555 560
 Gly Glu Lys Pro Tyr Glu Cys Ile Glu Cys Gly Lys Ala Phe Ser Asp
 565 570 575
 Gly Ser Tyr Leu Val Gln His Pro Arg Leu His Ser Gly Lys Arg Pro
 580 585 590
 Tyr Glu Cys Leu Glu Cys Gly Lys Ala Phe Arg Gln Arg Ala Ser Leu
 595 600 605
 Ile Cys His Gln Arg Cys His Thr Gly Glu Lys Pro Tyr Glu Cys Asn
 610 615 620
 Val Cys Gly Lys Ala Phe Ser His Arg Lys Ser Leu Thr Leu His Gln
 625 630 635 640
 Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu Cys Ser Lys
 645 650 655
 Ala Phe Ser Gln Val Ala His Leu Thr Leu His Lys Arg Ile His Thr
 660 665 670
 Gly Glu Arg Pro Tyr Glu Cys Lys Glu Cys Gly Lys Ala Phe Arg Gln
 675 680 685
 Ser Val His Leu Ala His His Gln Arg Ile His Thr Gly Glu Ser Ser
 690 695 700
 Val Ile Leu Ser Ser Ala Leu Pro Tyr His Gln Val Leu
 705 710 715

<210> 3
 <211> 2143
 <212> DNA
 <213> Homo sapiens

<400> 3
 gggagtttctt gcaattccag aaccatgact gatgggttgg tgacattcag ggatgtggcc 60
 atcgacttct ctcaggagga gtgggaatgc ctggaccctg ctcagagggga cttgtacgtg 120
 gatgtaatgt tggagaacta tagtaacttg gtgtcactgg atttggagtc aaaaacgtat 180
 gagaccaaaa aatatttttc agaaaatgat atttttgaaa taaatttttc ccagtgggag 240
 atgaaggaca aaagtaaaac ccttggcctt gaggcattcca tcttcagaaa taattggaag 300
 tgcaaaagca tattcgaggg actaaaagga catcaagagg gatacttcag tcaaatgata 360
 atcagctatg aaaaaatacc ttcttacaga aaaagtaaat ctcttactcc acatcaaaga 420
 attcataata cagagaaatc ctatgtttgt aaggaatgtg ggaaggcttg cagtcattggc 480
 tcaaaacttg ttcaacatga gagaactcat acagctgaaa agcactttga atgtaaagaa 540
 tgtgggaaga attatttaag tgcctatcaa ctcaatgtgc atcagagatt tcatactggt 600
 gagaaaccct atgagtgtaa ggaatgtggg aagaccttta gctggggatc aagccttgtt 660
 aaacatgaga gaattcacac tggtagagaa ccctatgaat gtaaagaatg tgggaaggcc 720

```

tttagtcgtg gctatcacct tacccaacat cagaaaaattc atattggtgt gaaatccttat 780
aaatgtaagg aatgtgggaa ggcctttttt tggggctcaa gccttgctaa acatgagata 840
attcatcacg gtgagaaacc ttataaatgt aaagaatgtg ggaaggcctt cagtcgtggc 900
tatcaactta ctcagcatca gaaaatccat actggtgaaga aaccttatga atgtaaaata 960
tgtggaaagg ctttttggtg gggctatcaa cttactcgac atcagatatt tcatactggt 1020
gagaaaccct atgaatgcaa ggaatgtggg aaggccttta attgcggatc aagtccttatt 1080
caacatgaaa gaattcatatc tggtgagaaa ccttatgaat gtaaagaatg tggaaaggcc 1140
tttagtcgtg gctatcacct ttctcaacat cagaaaaatcc atactggtga gaaacctttt 1200
gaatgtaagg aatgtgggaa ggccttttagt tggggttcaa gccttggtta acatgagaga 1260
gttcatactg gtgagaaatc ccatgaatgt aaagaatgag gaaagacctt ttgtagtggg 1320
tatcaactta ctcagcatca ggtattttcac actggtgaga aaccttatga atgtagggaa 1380
tgtgggaagg cttttaattg tggatcaagc cttgttcaac atgaaagaat ccatacaggg 1440
gagaaaccct atgaatgtaa agaatgtgga aggccttttag tcgtggctat caccttactc 1500
aacatcagaa aattcatacc ggtgagaaac ctttcaaagt taaggaatgt gggaaggcct 1560
tcagttgggg ttcaagccta gtttaagcatg agagagtcca tactaatgag aagtccttatg 1620
aatgtaaaag ctgtgggaa ggcctttggtg gtggctatca acttagtggt catcagagat 1680
ttcatactgg tgagaagcct tatcaacata aggaattcgg gaagaccttt actcgtggct 1740
caaaacttgt tcatgagaga actcatagta atgataaacc ctacaaatat aacgaatgtg 1800
gggaagcctt tctgtggaca acttactcaa atgagaaaat tgatactgat gaaaccttat 1860
gattgaaagt tgtaaaagaa tattttgtgt gtgcgtatag acaacttatc ataataagaa 1920
ctcttactct tgagaaacct tgtgaatgta agggttgtgc aaaagccatt catttctggt 1980
tatgggcaat tatcttgcta tccagcaatt catactagtg agaaatattt tgaatataat 2040
taatatgaaa aggccttttag acttctgtac agtccttattg gatatcaatt tatactgatg 2100
taaaatcatt taaatgaaaa aaaaaaaaaa aaaaaaaaaa aaa 2143

```

<210> 4

<211> 518

<212> PRT

<213> Homo sapiens

<400> 4

```

Met Thr Asp Gly Leu Val Thr Phe Arg Asp Val Ala Ile Asp Phe Ser
 1             5             10             15

Gln Glu Glu Trp Glu Cys Leu Asp Pro Ala Gln Arg Asp Leu Tyr Val
      20             25             30

Asp Val Met Leu Glu Asn Tyr Ser Asn Leu Val Ser Leu Asp Leu Glu
      35             40             45

Ser Lys Thr Tyr Glu Thr Lys Lys Ile Phe Ser Glu Asn Asp Ile Phe
      50             55             60

Glu Ile Asn Phe Ser Gln Trp Glu Met Lys Asp Lys Ser Lys Thr Leu
      65             70             75             80

Gly Leu Glu Ala Ser Ile Phe Arg Asn Asn Trp Lys Cys Lys Ser Ile
      85             90             95

Phe Glu Gly Leu Lys Gly His Gln Glu Gly Tyr Phe Ser Gln Met Ile
      100            105            110

Ile Ser Tyr Glu Lys Ile Pro Ser Tyr Arg Lys Ser Lys Ser Leu Thr
      115            120            125

Pro His Gln Arg Ile His Asn Thr Glu Lys Ser Tyr Val Cys Lys Glu
      130            135            140

```

Cys Gly Lys Ala Cys Ser His Gly Ser Lys Leu Val Gln His Glu Arg
 145 150 155 160
 Thr His Thr Ala Glu Lys His Phe Glu Cys Lys Glu Cys Gly Lys Asn
 165 170 175
 Tyr Leu Ser Ala Tyr Gln Leu Asn Val His Gln Arg Phe His Thr Gly
 180 185 190
 Glu Lys Pro Tyr Glu Cys Lys Glu Cys Gly Lys Thr Phe Ser Trp Gly
 195 200 205
 Ser Ser Leu Val Lys His Glu Arg Ile His Thr Gly Glu Lys Pro Tyr
 210 215 220
 Glu Cys Lys Glu Cys Gly Lys Ala Phe Ser Arg Gly Tyr His Leu Thr
 225 230 235 240
 Gln His Gln Lys Ile His Ile Gly Val Lys Ser Tyr Lys Cys Lys Glu
 245 250 255
 Cys Gly Lys Ala Phe Phe Trp Gly Ser Ser Leu Ala Lys His Glu Ile
 260 265 270
 Ile His Thr Gly Glu Lys Pro Tyr Lys Cys Lys Glu Cys Gly Lys Ala
 275 280 285
 Phe Ser Arg Gly Tyr Gln Leu Thr Gln His Gln Lys Ile His Thr Gly
 290 295 300
 Lys Lys Pro Tyr Glu Cys Lys Ile Cys Gly Lys Ala Phe Cys Trp Gly
 305 310 315 320
 Tyr Gln Leu Thr Arg His Gln Ile Phe His Thr Gly Glu Lys Pro Tyr
 325 330 335
 Glu Cys Lys Glu Cys Gly Lys Ala Phe Asn Cys Gly Ser Ser Leu Ile
 340 345 350
 Gln His Glu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu
 355 360 365
 Cys Gly Lys Ala Phe Ser Arg Gly Tyr His Leu Ser Gln His Gln Lys
 370 375 380
 Ile His Thr Gly Glu Lys Pro Phe Glu Cys Lys Glu Cys Gly Lys Ala
 385 390 395 400
 Phe Ser Trp Gly Ser Ser Leu Val Lys His Glu Arg Val His Thr Gly
 405 410 415
 Glu Lys Ser His Glu Cys Lys Glu Cys Gly Lys Thr Phe Cys Ser Gly
 420 425 430
 Tyr Gln Leu Thr Arg His Gln Val Phe His Thr Gly Glu Lys Pro Tyr
 435 440 445

Glu Cys Lys Glu Cys Gly Lys Ala Phe Asn Cys Gly Ser Ser Leu Val
 450 455 460

Gln His Glu Arg Ile His Thr Gly Glu Lys Pro Tyr Glu Cys Lys Glu
 465 470 475 480

Cys Gly Arg Leu Leu Val Val Ala Ile Thr Leu Leu Asn Ile Arg Lys
 485 490 495

Phe Ile Pro Val Arg Asn Leu Ser Asn Val Arg Asn Val Gly Arg Pro
 500 505 510

Ser Val Gly Val Gln Ala
 515

<210> 5
 <211> 18
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide)

<220>
 <221> modified_base
 <222> (6)
 <223> A, C, T or G

<220>
 <221> modified_base
 <222> (9)
 <223> A, T, C of G

<220>
 <221> modified_base
 <222> (18)
 <223> A, T, C or G

<400> 5
 cayacnggng araarccn

18

<210> 6
 <211> 6
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 probe

<400> 6
 His Thr Gly Glu Lys Pro
 1 5

<210> 7
 <211> 47
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Synthetic
 oligonucleotide

<220>
 <221> MOD_RES
 <222> (1)
 <223> Tyr or Phe

<220>
 <221> MOD_RES
 <222> (2)
 <223> essential amino acid

<220>
 <221> MOD_RES
 <222> (4)..(27)
 <223> essential amino acid

<220>
 <221> MOD_RES
 <222> (29)..(31)
 <223> essential amino acid

<220>
 <221> MOD_RES
 <222> (33)..(37)
 <223> essential amino acid

<220>
 <221> MOD_RES
 <222> (39)..(40)
 <223> essential amino acid

<220>
 <221> MOD_RES
 <222> (42)..(46)
 <223> region may encompass 3-5 essential amino acids

<400> 7
 Xaa Xaa Cys Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa
 1 5 10 15

Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Cys Xaa Xaa Xaa Phe
 20 25 30

Xaa Xaa Xaa Xaa Xaa Leu Xaa Xaa His Xaa Xaa Xaa Xaa Xaa His
 35 40 45